

SEQUENCE LISTING

<110> Reppert, Steven M.  
Ebisawa, Takashi

<120> HIGH-AFFINITY MELATONIN RECEPTOR AND USES THEREOF

<130> 10217/250003

<140> US 09/226,046  
<141> 1999-01-03

<150> US 08/466,103  
<151> 1995-06-06

<150> US 08/319,887  
<151> 1994-10-07

<150> US 08/261,857  
<151> 1994-06-17

<160> 29

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<220>  
<221> CDS  
<222> (32)...(1291)

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52

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tgc ttg gat tgc agg aca cct ggt acc ata cga aca gag cag gat gca  
Cys Leu Asp Cys Arg Thr Pro Gly Thr Ile Arg Thr Glu Gln Asp Ala  
10 15 20

100

cag gac agc gca tct cag gga ctc acc tct gcc ctg gcg gtg gtt ctt  
Gln Asp Ser Ala Ser Gln Gly Leu Thr Ser Ala Leu Ala Val Val Leu  
25 30 35

148

ata ttc acc att gtt gtg gat gtc ctg ggc aat ata ttg gtc att ttg  
Ile Phe Thr Ile Val Val Asp Val Leu Gly Asn Ile Leu Val Ile Leu  
40 45 50 55

196

tct gtc ctg agg aac aag ctg cag aat gct gga aat ctc ttt gtt  
Ser Val Leu Arg Asn Lys Lys Leu Gln Asn Ala Gly Asn Leu Phe Val  
60 65 70

244

gtc agt ttg tct att gcc gat ctg gtt gct gtg tat ccc tat ccg  
Val Ser Leu Ser Ile Ala Asp Leu Val Val Ala Val Tyr Pro Tyr Pro  
75 80 85

292

gtc att ctc ata gct att ttc cag aat gga tgg acg ctt gga aat atc  
Val Ile Leu Ile Ala Ile Phe Gln Asn Gly Trp Thr Leu Gly Asn Ile  
90 95 100

340

cat tgt cag atc agt ggc ttc ctg atg gga ctc agc gtt att gga tca His Cys Gln Ile Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser 105 110 115	388
gtc ttc aac ata aca gcc ata gct atc aac agg tat tgc tac atc tgc Val Phe Asn Ile Thr Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys 120 125 130 135	436
cac agc ctg aga tat gac aag ctt tat aat caa aga agc acc tgg tgc His Ser Leu Arg Tyr Asp Lys Leu Tyr Asn Gln Arg Ser Thr Trp Cys 140 145 150	484
tac ctt ggc ctg aca tgg ata cta act ata att gca atc gtg cca aac Tyr Leu Gly Leu Thr Trp Ile Leu Thr Ile Ile Ala Ile Val Pro Asn 155 160 165	532
ttt ttt gtt gga tca cta cag tat gac ccc agg att ttt tct tgc aca Phe Phe Val Gly Ser Leu Gln Tyr Asp Pro Arg Ile Phe Ser Cys Thr 170 175 180	580
ttt gcg cag aca gtg agt tcc tca tac acc ata aca gta gtg gtg gtg Phe Ala Gln Thr Val Ser Ser Tyr Thr Ile Thr Val Val Val Val 185 190 195	628
cat ttt ata gtc cct ctt agt gtt gtc aca ttc tgt tac tta aga ata His Phe Ile Val Pro Leu Ser Val Val Thr Phe Cys Tyr Leu Arg Ile 200 205 210 215	676
tgg gtt tta gtc aca gaa cac aga gtt aga caa gac ttc aag Trp Val Leu Val Ile Gln Val Lys His Arg Val Arg Gln Asp Phe Lys 220 225 230	724
caa aag ttg aca caa aca gac ttg aga aat ttc ttg acc atg ttt gtc Gln Lys Leu Thr Gln Thr Asp Leu Arg Asn Phe Leu Thr Met Phe Val 235 240 245	772
gtc ttt gta ctt ttt gca gtt tgc tgg gcc ccc tta aac ttt atc ggc Val Phe Val Leu Phe Ala Val Cys Trp Ala Pro Leu Asn Phe Ile Gly 250 255 260	820
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tgg ctg ttt gtt tta agc tat ttc atg gcc tat ttt aac agt tgt ctc Trp Leu Phe Val Leu Ser Tyr Phe Met Ala Tyr Phe Asn Ser Cys Leu 280 285 290 295	916
aat gct gtt ata tat ggt gtg cta aat caa aac ttc cgc aag gag tac Asn Ala Val Ile Tyr Gly Val Leu Asn Gln Asn Phe Arg Lys Glu Tyr 300 305 310	964
aaa aga ata ctg atg tcc tta ttg act cca aga ctg ttg ttt ctt gac Lys Arg Ile Leu Met Ser Leu Leu Thr Pro Arg Leu Leu Phe Leu Asp 315 320 325	1012
aca tct aga gga gga act gag gga ttg aaa agt aag cct tcg cca gct Thr Ser Arg Gly Gly Thr Glu Gly Leu Lys Ser Lys Pro Ser Pro Ala 330 335 340	1060

gta acc aac aac aat caa gca gat atg cta gga gaa gca agg tca ctg 1108  
 Val Thr Asn Asn Asn Gln Ala Asp Met Leu Gly Glu Ala Arg Ser Leu  
 345 350 355  
 tgg ctg agc agg aga aat ggt gcg aaa atg gtg atc atc atc agg cca 1156  
 Trp Leu Ser Arg Arg Asn Gly Ala Lys Met Val Ile Ile Ile Arg Pro  
 360 365 370 375  
 aga aaa gca caa att gca atc atc cat caa ata ttc tgg cct cag agt 1204  
 Arg Lys Ala Gln Ile Ala Ile Ile His Gln Ile Phe Trp Pro Gln Ser  
 380 385 390  
 tca tgg gca aca tgc cgt caa gac aca aag att acc gga gaa gat 1252  
 Ser Trp Ala Thr Cys Arg Gln Asp Thr Lys Ile Thr Gly Glu Glu Asp  
 395 400 405  
 ggc tgc cgt gaa ctg tgc aag gac ggg att tcc caa agg tgagacccaa 1301  
 Gly Cys Arg Glu Leu Cys Lys Asp Gly Ile Ser Gln Arg  
 410 415 420  
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 <213> Xenopus laevis  
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 Ser Ala Leu Ala Val Val Leu Ile Phe Thr Ile Val Val Asp Val Leu 35 40 45  
 Gly Asn Ile Leu Val Ile Leu Ser Val Leu Arg Asn Lys Lys Leu Gln 50 55 60  
 Asn Ala Gly Asn Leu Phe Val Val Ser Leu Ser Ile Ala Asp Leu Val 65 70 75 80  
 Val Ala Val Tyr Pro Tyr Pro Val Ile Leu Ile Ala Ile Phe Gln Asn 85 90 95  
 Gly Trp Thr Leu Gly Asn Ile His Cys Gln Ile Ser Gly Phe Leu Met 100 105 110  
 Gly Leu Ser Val Ile Gly Ser Val Phe Asn Ile Thr Ala Ile Ala Ile 115 120 125  
 Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Arg Tyr Asp Lys Leu Tyr 130 135 140  
 Asn Gln Arg Ser Thr Trp Cys Tyr Leu Gly Leu Thr Trp Ile Leu Thr 145 150 155 160  
 Ile Ile Ala Ile Val Pro Asn Phe Phe Val Gly Ser Leu Gln Tyr Asp 165 170 175  
 Pro Arg Ile Phe Ser Cys Thr Phe Ala Gln Thr Val Ser Ser Tyr 180 185 190  
 Thr Ile Thr Val Val Val His Phe Ile Val Pro Leu Ser Val Val 195 200 205  
 Thr Phe Cys Tyr Leu Arg Ile Trp Val Leu Val Ile Gln Val Lys His 210 215 220  
 Arg Val Arg Gln Asp Phe Lys Gln Lys Leu Thr Gln Thr Asp Leu Arg 225 230 235 240  
 Asn Phe Leu Thr Met Phe Val Val Phe Val Leu Phe Ala Val Cys Trp 245 250 255  
 Ala Pro Leu Asn Phe Ile Gly Leu Ala Val Ala Ile Asn Pro Phe His 260 265 270

<210> 3

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<212> DNA

<213> Ovis

<220>

<221> CDS

$\langle 222 \rangle (49) \dots (1140)$

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 Met Ala Gly  
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57

cgg ctg tgg ggc tcg ccg ggc ggg acc ccc aag ggc aac ggc agc agc  
 Arg Leu Trp Gly Ser Pro Gly Gly Thr Pro Lys Gly Asn Gly Ser Ser  
 5 10 15

105

Arg Leu Ile 10  
 5 gcg ctg ctc aac gtc tcg cag gcg gcg ccc ggc gcc ggg gac ggt gtg  
 Ala Leu Leu Asn Val Ser Gln Ala Ala Pro Gly Ala Gly Asp Gly Val 35  
 20 25 30  
 gct gcc tcc atc ctc atc

153

20 25 30 35 40 45 50  
 cg<sup>g</sup> cc<sup>g</sup> cc<sup>g</sup> cc<sup>c</sup> tc<sup>g</sup> tg<sup>g</sup> ct<sup>g</sup> gc<sup>c</sup> gc<sup>c</sup> ac<sup>c</sup> ct<sup>c</sup> gc<sup>c</sup> tc<sup>c</sup> at<sup>c</sup> ct<sup>c</sup> at<sup>c</sup>  
 Arg Pro Arg Pro Ser Trp Leu Ala Ala Thr Leu Ala Ser Ile Leu Ile  
 40 45 50

201

251

70 agc ctg gca gtt gca gac ctg ctg gtg gcc gtg tat ccg tac ccc ttg  
 Ser Leu Ala Val Ala Asp Leu Leu Val Ala Val Tyr Pro Tyr Pro Leu  
 95  
 85

85 gcg ctg gcg tct ata gtt aac aat ggg tgg agc ctg agc tcc ctg cat  
 Ala Leu Ala Ser Ile Val Asn Asn Gly Trp Ser Leu Ser Ser Leu His 115  
 100 105 110

393

tgc caa ctt agt ggc ttc ctg atg ggc ttg agc gtc atc ggg tcc gtt Cys Gln Leu Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser Val 120 125 130	441
ttc agc atc acg gga att gcc atc aac cgc tat tgc tgc atc tgc cac Phe Ser Ile Thr Gly Ile Ala Ile Asn Arg Tyr Cys Cys Ile Cys His 135 140 145	489
agc ctc aga tac ggc aag ctg tat agc ggc acg aat tcc ctc tgc tac Ser Leu Arg Tyr Gly Lys Leu Tyr Ser Gly Thr Asn Ser Leu Cys Tyr 150 155 160	537
gtg ttc ctg atc tgg acg ctg acg ctc gtg gcg atc gtg ccc aac ctg Val Phe Leu Ile Trp Thr Leu Thr Leu Val Ala Ile Val Pro Asn Leu 165 170 175	585
tgt gtg ggg acc ctg cag tac gac ccg agg atc tat tcc tgt acc ttc Cys Val Gly Thr Leu Gln Tyr Asp Pro Arg Ile Tyr Ser Cys Thr Phe 180 185 190 195	633
acg cag tcc gtc agc tca gcc tac acg atc gcc gtg gtg ttc cat Thr Gln Ser Val Ser Ala Tyr Thr Ile Ala Val Val Val Phe His 200 205 210	681
ttc ata gtt ccg atg ctc gta gtc ttc tgt tac ctg aga atc tgg Phe Ile Val Pro Met Leu Val Val Val Phe Cys Tyr Leu Arg Ile Trp 215 220 225	729
gcc ctg gtt ctt cag gtc aga tgg aag gtg aaa ccg gac aac aaa ccg Ala Leu Val Leu Gln Val Arg Trp Lys Val Lys Pro Asp Asn Lys Pro 230 235 240	777
aaa ctg aag ccc cag gac ttc agg aat ttt gtc acc atg ttt gtg gtt Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met Phe Val Val 245 250 255	825
ttt gtc ctc ttt gcc att tgc tgg gct cct ctg aac ttc att ggt ctc Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu Asn Phe Ile Gly Leu 260 265 270 275	873
gtt gtg gcc tcg gac ccc gcc agc atg gca ccc agg atc ccc gag tgg Val Val Ala Ser Asp Pro Ala Ser Met Ala Pro Arg Ile Pro Glu Trp 280 285 290	921
ctg ttt gtg gct agt tac tat atg gca tat ttc aac agc tgc ctc aat Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe Asn Ser Cys Leu Asn 295 300 305	969
gcg atc ata tat gga cta ctg aac caa aat ttc agg cag gaa tac aga Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn Phe Arg Gln Glu Tyr Arg 310 315 320	1017
aaa att ata gtc tca ttg tgt acc acc aag atg ttc ttt gtg gat agc Lys Ile Ile Val Ser Leu Cys Thr Lys Met Phe Phe Val Asp Ser 325 330 335	1065
tcc aat cat gta gca gat aga att aaa cgc aaa ccc tct cca tta ata Ser Asn His Val Ala Asp Arg Ile Lys Arg Lys Pro Ser Pro Leu Ile 340 345 350 355	1113

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 <212> PRT  
 <213> Ovis

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 Asp Gly Val Arg Pro Arg Pro Ser Trp Leu Ala Ala Thr Leu Ala Ser  
 35 40 45  
 Ile Leu Ile Phe Thr Ile Val Val Asp Ile Val Gly Asn Leu Leu Val  
 50 55 60  
 Val Leu Ser Val Tyr Arg Asn Lys Lys Leu Arg Asn Ala Gly Asn Val  
 65 70 75 80  
 Phe Val Val Ser Leu Ala Val Ala Asp Leu Leu Val Ala Val Tyr Pro  
 85 90 95  
 Tyr Pro Leu Ala Leu Ala Ser Ile Val Asn Asn Gly Trp Ser Leu Ser  
 100 105 110  
 Ser Leu His Cys Gln Leu Ser Gly Phe Leu Met Gly Leu Ser Val Ile  
 115 120 125  
 Gly Ser Val Phe Ser Ile Thr Gly Ile Ala Ile Asn Arg Tyr Cys Cys  
 130 135 140  
 Ile Cys His Ser Leu Arg Tyr Gly Lys Leu Tyr Ser Gly Thr Asn Ser  
 145 150 155 160  
 Leu Cys Tyr Val Phe Leu Ile Trp Thr Leu Thr Leu Val Ala Ile Val  
 165 170 175  
 Pro Asn Leu Cys Val Gly Thr Leu Gln Tyr Asp Pro Arg Ile Tyr Ser  
 180 185 190  
 Cys Thr Phe Thr Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala Val Val  
 195 200 205  
 Val Phe His Phe Ile Val Pro Met Leu Val Val Val Phe Cys Tyr Leu  
 210 215 220  
 Arg Ile Trp Ala Leu Val Leu Gln Val Arg Trp Lys Val Lys Pro Asp  
 225 230 235 240  
 Asn Lys Pro Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met  
 245 250 255  
 Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu Asn Phe  
 260 265 270  
 Ile Gly Leu Val Val Ala Ser Asp Pro Ala Ser Met Ala Pro Arg Ile  
 275 280 285  
 Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe Asn Ser  
 290 295 300  
 Cys Leu Asn Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn Phe Arg Gln  
 305 310 315 320  
 Glu Tyr Arg Lys Ile Ile Val Ser Leu Cys Thr Thr Lys Met Phe Phe  
 325 330 335  
 Val Asp Ser Ser Asn His Val Ala Asp Arg Ile Lys Arg Lys Pro Ser  
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 Pro Leu Ile Ala Asn His Asn Leu Ile Lys Val Asp Ser Val  
 355 360 365

<210> 5  
 <211> 867  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(864)

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att tat ccg tac ccg ttg gtg ctg atg tcg ata ttt aac aac ggg tgg Ile Tyr Pro Tyr Pro Leu Val Leu Met Ser Ile Phe Asn Asn Gly Trp 20 25 30	96
aac ctg ggc tat ctg cac tgc caa gtc agt ggg ttc ctg atg ggc ctg Asn Leu Gly Tyr Leu His Cys Gln Val Ser Gly Phe Leu Met Gly Leu 35 40 45	144
agc gtc atc ggc tcc ata ttc aac atc acc ggc atc gac aac cgc Ser Val Ile Gly Ser Ile Phe Asn Ile Thr Gly Ile Ala Ile Asn Arg 50 55 60	192
tac tgt tac atc tgc cac agt ctc aag tgc gac aaa ctg tac agc agc Tyr Cys Tyr Ile Cys His Ser Leu Lys Cys Asp Lys Leu Tyr Ser Ser 65 70 75 80	240
aag aac tcc ctc tgc tac gtg ctc ctc ata tgg ctc ctg acg ggc Lys Asn Ser Leu Cys Tyr Val Leu Leu Ile Trp Leu Leu Thr Ala Ala 85 90 95	288
gtc ctg ccc aac ctc cgt cgt ggg act ctc cag tac gag ccg agg atc Val Leu Pro Asn Leu Arg Arg Gly Thr Leu Gln Tyr Glu Pro Arg Ile 100 105 110	336
tac tcg tgc acc ttc gcc cag tcc gtc agc tcc gcc tac acc atc gcc Tyr Ser Cys Thr Phe Ala Gln Ser Val Ser Ala Tyr Thr Ile Ala 115 120 125	384
gtg gtg gtt ttc cac ttc ctc gtc ccc atg atc ata gtc atc ttc tgt Val Val Val Phe His Phe Leu Val Pro Met Ile Ile Val Ile Phe Cys 130 135 140	432
tac ctg aga ata tgg atc ctg gtt ctc cag gtc aga cag agg gtg aaa Tyr Leu Arg Ile Trp Ile Leu Val Leu Gln Val Arg Gln Arg Val Lys 145 150 155 160	480
cct gac cgc aaa ccc aaa ctg aaa cca cac gac ttc agg aat ttt gtc Pro Asp Arg Lys Pro Lys Leu Lys Pro His Asp Phe Arg Asn Phe Val 165 170 175	528
acc atg ttt gtg gtt ttt gtc ctt ttt gcc att tgc tgg gct cct ctg Thr Met Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu 180 185 190	576
aac ttc att ggc ctg gcc gtg gcc tct gac ccc gcc agc atg gtg cct Asn Phe Ile Gly Leu Ala Val Ala Ser Asp Pro Ala Ser Met Val Pro 195 200 205	624
agg atc cca gag tgg ctg ttt gtg gcc agt tac tac atg ggc tat ttc Arg Ile Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe 210 215 220	672

aac agc tgc ctc aat gcc att ata tcg ggc tac tgg aac caa aat ttc 720  
 Asn Ser Cys Leu Asn Ala Ile Ile Ser Gly Tyr Trp Asn Gln Asn Phe  
 225 230 235 240  
 agg aag gaa tac agg aga att ata gtc tgc ctc gtg aca gcc agg gtg 768  
 Arg Lys Glu Tyr Arg Arg Ile Ile Val Ser Leu Val Thr Ala Arg Val  
 245 250 255  
 ttc ttt gtg gac agc tct aac gac gtg gcc gat agg gtt aaa tgg aaa 816  
 Phe Phe Val Asp Ser Ser Asn Asp Val Ala Asp Arg Val Lys Trp Lys  
 260 265 270  
 ccg tct cca ctg atg acc aac aat aat gta gta aag gtg gac tcc gtt 864  
 Pro Ser Pro Leu Met Thr Asn Asn Val Val Lys Val Asp Ser Val  
 275 280 285  
 867

taa

<210> 6  
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 <212> PRT  
 <213> Homo sapiens

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 Ile Tyr Pro Tyr Pro Leu Val Leu Met Ser Ile Phe Asn Asn Gly Trp 30  
 20 25  
 Asn Leu Gly Tyr Leu His Cys Gln Val Ser Gly Phe Leu Met Gly Leu 45  
 35 40  
 Ser Val Ile Gly Ser Ile Phe Asn Ile Thr Gly Ile Ala Ile Asn Arg 60  
 50 55  
 Tyr Cys Tyr Ile Cys His Ser Leu Lys Cys Asp Lys Leu Tyr Ser Ser 80  
 65 70 75  
 Lys Asn Ser Leu Cys Tyr Val Leu Leu Ile Trp Leu Leu Thr Ala Ala 95  
 85 90  
 Val Leu Pro Asn Leu Arg Arg Gly Thr Leu Gln Tyr Glu Pro Arg Ile 110  
 100 105  
 Tyr Ser Cys Thr Phe Ala Gln Ser Val Ser Ala Tyr Thr Ile Ala 125  
 115 120  
 Val Val Val Phe His Phe Leu Val Pro Met Ile Ile Val Ile Phe Cys 140  
 130 135  
 Tyr Leu Arg Ile Trp Ile Leu Val Leu Gln Val Arg Gln Arg Val Lys 160  
 145 150 155  
 Pro Asp Arg Lys Pro Lys Leu Lys Pro His Asp Phe Arg Asn Phe Val 175  
 165 170  
 Thr Met Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu 190  
 180 185  
 Asn Phe Ile Gly Leu Ala Val Ala Ser Asp Pro Ala Ser Met Val Pro 205  
 195 200  
 Arg Ile Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe 220  
 210 215  
 Asn Ser Cys Leu Asn Ala Ile Ile Ser Gly Tyr Trp Asn Gln Asn Phe 240  
 225 230 235  
 Arg Lys Glu Tyr Arg Arg Ile Ile Val Ser Leu Val Thr Ala Arg Val 255  
 245 250  
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 260 265  
 Pro Ser Pro Leu Met Thr Asn Asn Val Val Lys Val Asp Ser Val 285  
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<220>  
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 <223> Xaa = Any Amino Acid

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 Asn Pro Xaa Xaa Tyr  
 1 5

<210> 8  
 <211> 7  
 <212> PRT  
 <213> Xenopus laevis

<400> 8  
 Ala Ile Ala Ile Asn Arg Tyr  
 1 5

<210> 9  
 <211> 8  
 <212> PRT  
 <213> Xenopus laevis

<400> 9  
 Phe Ala Val Cys Trp Ala Pro Leu  
 1 5

<210> 10  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 1 5

<210> 11  
 <211> 1085  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (33)...(1082)

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tcg tgg ctg gcg tcc gcc cta gcc tgc gtc ctc atc ttc acc atc gtg Ser Trp Leu Ala Ser Ala Leu Ala Cys Val Leu Ile Phe Thr Ile Val 25 30 35	149
gtg gac atc ctg ggc aac ctc ctg gtc atc ctg tgc gtg tat cgg aac Val Asp Ile Leu Gly Asn Leu Leu Val Ile Leu Ser Val Tyr Arg Asn 40 45 50 55	197
aag aag ctc agg aac gca gga aac atc ttt gtg gtg agc tta gcg gtg Lys Lys Leu Arg Asn Ala Gly Asn Ile Phe Val Val Ser Leu Ala Val 60 65 70	245
gca gac ctg gtg gtc att tat ccg tac ccg ttg gtg ctg atg tcg Ala Asp Leu Val Val Ala Ile Tyr Pro Tyr Pro Leu Val Leu Met Ser 75 80 85	293
ata ttt aac aac ggg tgg aac ctg ggc tat ctg cac tgc caa gtc agt Ile Phe Asn Asn Gly Trp Asn Leu Gly Tyr Leu His Cys Gln Val Ser 90 95 100	341
ggg ttc ctg atg ggc ctg agc gtc atc ggc tcc ata ttc aac atc acc Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser Ile Phe Asn Ile Thr 105 110 115	389
ggc atc gcc atc aac cgc tac tgc tac atc tgc cac agt ctc aag tac Gly Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Lys Tyr 120 125 130 135	437
gac aaa ctg tac agc agc aag aac tcc ctc tgc tac gtg ctc ctc ata Asp Lys Leu Tyr Ser Ser Lys Asn Ser Leu Cys Tyr Val Leu Leu Ile 140 145 150	485
tgg ctc ctg acg ctg gcg gtc ctg ccc aac ctc cgt gca ggg act Trp Leu Leu Thr Leu Ala Ala Val Leu Pro Asn Leu Arg Ala Gly Thr 155 160 165	533
ctc cag tac gac ccg agg atc tac tgc tgc acc ttc gcc cag tcc gtc Leu Gln Tyr Asp Pro Arg Ile Tyr Ser Cys Thr Phe Ala Gln Ser Val 170 175 180	581
agc tcc gcc tac acc atc gcc gtg gtg gtt ttc cac ttc ctc gtc ccc Ser Ser Ala Tyr Thr Ile Ala Val Val Val Phe His Phe Leu Val Pro 185 190 195	629
atg atc ata gtc atc ttc tgt tac ctg aga ata tgg atc ctg gtt ctc Met Ile Ile Val Ile Phe Cys Tyr Leu Arg Ile Trp Ile Leu Val Leu 200 205 210 215	677
cag gtc aga cag agg gtg aaa cct gac cgc aaa ccc aaa ctg aaa cca Gln Val Arg Gln Arg Val Lys Pro Asp Arg Lys Pro Lys Leu Lys Pro 220 225 230	725
cag gac ttc agg aat ttt gtc acc atg ttt gtg gtt ttt gtc ctc ttt Gln Asp Phe Arg Asn Phe Val Thr Met Phe Val Val Phe Val Leu Phe 235 240 245	773

gcc att tgc tgg gct cct ctg aac ttc att ggc ctg gcc gtg gcc tct Ala Ile Cys Trp Ala Pro Leu Asn Phe Ile Gly Leu Ala Val Ala Ser 250 255 260	821
gac ccc gcc agc atg gtg cct agg atc cca gag tgg ctg ttt gtg gcc Asp Pro Ala Ser Met Val Pro Arg Ile Pro Glu Trp Leu Phe Val Ala 265 270 275	869
agt tac tac atg gcg tat ttc aac agc tgc ctc aat gcc att ata tac Ser Tyr Tyr Met Ala Tyr Phe Asn Ser Cys Leu Asn Ala Ile Ile Tyr 280 285 290 295	917
ggg cta ctg aac caa aat ttc agg aag gaa tac agg aga att ata gtc Gly Leu Leu Asn Gln Asn Phe Arg Lys Glu Tyr Arg Arg Ile Ile Val 300 305 310	965
tcg ctc tgt aca gcc agg gtg ttc ttt gtg gac agc tct aac gac gtg Ser Leu Cys Thr Ala Arg Val Phe Phe Val Asp Ser Ser Asn Asp Val 315 320 325	1013
gcc gat agg gtt aaa tgg aaa ccg tct cca ctg atg acc aac aat aat Ala Asp Arg Val Lys Trp Lys Pro Ser Pro Leu Met Thr Asn Asn Asn 330 335 340	1061
gta gta aag gtg gac tcc gtt taa Val Val Lys Val Asp Ser Val 345 350	1085

<210> 12  
 <211> 350  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Gln Gly Asn Gly Ser Ala Leu Pro Asn Ala Ser Gln Pro Val Leu  
 1 5 10 15  
 Arg Gly Asp Gly Ala Arg Pro Ser Trp Leu Ala Ser Ala Leu Ala Cys  
 20 25 30  
 Val Leu Ile Phe Thr Ile Val Val Asp Ile Leu Gly Asn Leu Leu Val  
 35 40 45  
 Ile Leu Ser Val Tyr Arg Asn Lys Lys Leu Arg Asn Ala Gly Asn Ile  
 50 55 60  
 Phe Val Val Ser Leu Ala Val Ala Asp Leu Val Val Ala Ile Tyr Pro  
 65 70 75 80  
 Tyr Pro Leu Val Leu Met Ser Ile Phe Asn Asn Gly Trp Asn Leu Gly  
 85 90 95  
 Tyr Leu His Cys Gln Val Ser Gly Phe Leu Met Gly Leu Ser Val Ile  
 100 105 110  
 Gly Ser Ile Phe Asn Ile Thr Gly Ile Ala Ile Asn Arg Tyr Cys Tyr  
 115 120 125  
 Ile Cys His Ser Leu Lys Tyr Asp Lys Leu Tyr Ser Ser Lys Asn Ser  
 130 135 140  
 Leu Cys Tyr Val Leu Leu Ile Trp Leu Leu Thr Leu Ala Ala Val Leu  
 145 150 155 160  
 Pro Asn Leu Arg Ala Gly Thr Leu Gln Tyr Asp Pro Arg Ile Tyr Ser  
 165 170 175  
 Cys Thr Phe Ala Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala Val Val  
 180 185 190  
 Val Phe His Phe Leu Val Pro Met Ile Ile Val Ile Phe Cys Tyr Leu  
 195 200 205

Arg Ile Trp Ile Leu Val Leu Gln Val Arg Gln Arg Val Lys Pro Asp  
 210 215 220  
 Arg Lys Pro Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met  
 225 230 235 240  
 Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu Asn Phe  
 245 250 255  
 Ile Gly Leu Ala Val Ala Ser Asp Pro Ala Ser Met Val Pro Arg Ile  
 260 265 270  
 Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe Asn Ser  
 275 280 285  
 Cys Leu Asn Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn Phe Arg Lys  
 290 295 300  
 Glu Tyr Arg Arg Ile Ile Val Ser Leu Cys Thr Ala Arg Val Phe Phe  
 305 310 315 320  
 Val Asp Ser Ser Asn Asp Val Ala Asp Arg Val Lys Trp Lys Pro Ser  
 325 330 335  
 Pro Leu Met Thr Asn Asn Asn Val Val Lys Val Asp Ser Val  
 340 345 350

<210> 13  
 <211> 1062  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(1059)

<400> 13

atg aag ggc aat gtc agc gag ctg ctc aat gcc act cag cag gct cca	48
Met Lys Gly Asn Val Ser Glu Leu Leu Asn Ala Thr Gln Gln Ala Pro	
1 5 10 15	
ggc ggc ggg gag gga ggg aga cca cga ccg tcc tgg atg gcc tct aca	96
Gly Gly Gly Glu Gly Gly Arg Pro Arg Pro Ser Trp Met Ala Ser Thr	
20 25 30	
ctg gcc ttc atc ctc atc ttt acc atc gtg gtg gac att ctg ggc aac	144
Leu Ala Phe Ile Leu Ile Phe Thr Ile Val Val Asp Ile Leu Gly Asn	
35 40 45	
ctg ctg gtc atc ctg tct gtg tac cgc aac aag aag ctc agg aac tca	192
Leu Leu Val Ile Leu Ser Val Tyr Arg Asn Lys Lys Leu Arg Asn Ser	
50 55 60	
ggg aat ata ttt gtg gtg agt tta gct gtg gca gac ctc gtg gtg gct	240
Gly Asn Ile Phe Val Val Ser Leu Ala Val Ala Asp Leu Val Val Ala	
65 70 75 80	
gtt tac cct tat ccc ttg gtg ctg aca tct atc ctt aac aac gga tgg	288
Val Tyr Pro Tyr Pro Leu Val Leu Thr Ser Ile Leu Asn Asn Gly Trp	
85 90 95	
aat ctg gga tat cta cac tgt caa gtc agc gca ttt cta atg ggc ttg	336
Asn Leu Gly Tyr Leu His Cys Gln Val Ser Ala Phe Leu Met Gly Leu	
100 105 110	
agt gtc atc ggc tcg ata ttg aac atc acg ggg atc gct atg aac cgt	384
Ser Val Ile Gly Ser Ile Leu Asn Ile Thr Gly Ile Ala Met Asn Arg	
115 120 125	

tac tgc tac att tgc cac agc ctc aag tac gac aaa ata tac agt aac Tyr Cys Tyr Ile Cys His Ser Leu Lys Tyr Asp Lys Ile Tyr Ser Asn 130 135 140	432
aag aac tcg ctc tgc tac gtg ttc ctg ata tgg atg ctg aca ctc atc Lys Asn Ser Leu Cys Tyr Val Phe Leu Ile Trp Met Leu Thr Leu Ile 145 150 155 160	480
gcc atc atg ccc aac ctg caa acc gga aca ctc cag tac gat ccc cgg Ala Ile Met Pro Asn Leu Gln Thr Gly Thr Leu Gln Tyr Asp Pro Arg 165 170 175	528
atc tac tcc tgt acc ttc acc cag tct gtc agc tca gcg tac acg ata Ile Tyr Ser Cys Thr Phe Thr Gln Ser Val Ser Ala Tyr Thr Ile 180 185 190	576
gca gtg gtg gtt ttc cat ttc atc gtg cct atg att att gtc atc ttc Ala Val Val Val Phe His Phe Ile Val Pro Met Ile Ile Val Ile Phe 195 200 205	624
tgc tac tta agg ata tgg gtc ctg gtc ctt cag gtc aga cgg agg gtg Cys Tyr Leu Arg Ile Trp Val Leu Val Leu Gln Val Arg Arg Arg Val 210 215 220	672
aaa ccc gac aac aag ccc aaa ctg aag ccc cag gac ttc agg aac ttt Lys Pro Asp Asn Lys Pro Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe 225 230 235 240	720
gtc acc atg ttc gta gtt ttt gta ctt ttt gcc att tgt tgg gcc cca Val Thr Met Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro 245 250 255	768
ctc aac ctc ata ggt ctt att gtg gcc tca gac cct gcc acc atg gtc Leu Asn Leu Ile Gly Leu Ile Val Ala Ser Asp Pro Ala Thr Met Val 260 265 270	816
ccc agg atc cca gag tgg ctg ttc gtg gct agt tac tac ctg gcg tac Pro Arg Ile Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Leu Ala Tyr 275 280 285	864
ttc aac agc tgc ctc aac gca att ata tac gga cta ctg aat cag aat Phe Asn Ser Cys Leu Asn Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn 290 295 300	912
ttc aga aag gaa tac aaa aag att att gtc tcg ttg tgc aca gcc aag Phe Arg Lys Glu Tyr Lys Lys Ile Ile Val Ser Leu Cys Thr Ala Lys 305 310 315 320	960
atg ttc ttt gtg gag agt tca aat gaa gaa gca gat aag att aaa tgt Met Phe Phe Val Glu Ser Ser Asn Glu Ala Asp Lys Ile Lys Cys 325 330 335	1008
aag ccc tct cca cta ata ccc aat aat aac ttc ctc ccg gtg gac tct Lys Pro Ser Pro Leu Ile Pro Asn Asn Asn Phe Leu Pro Val Asp Ser 340 345 350	1056
gtt taa Val	1062

<210> 14  
<211> 353  
<212> PRT  
<213> Mus musculus

<400> 14  
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1 5 10 15  
Gly Gly Gly Glu Gly Arg Pro Arg Pro Ser Trp Met Ala Ser Thr  
20 25 30  
Leu Ala Phe Ile Leu Ile Phe Thr Ile Val Val Asp Ile Leu Gly Asn  
35 40 45  
Leu Leu Val Ile Leu Ser Val Tyr Arg Asn Lys Lys Leu Arg Asn Ser  
50 55 60  
Gly Asn Ile Phe Val Val Ser Leu Ala Val Ala Asp Leu Val Val Ala  
65 70 75 80  
Val Tyr Pro Tyr Pro Leu Val Leu Thr Ser Ile Leu Asn Asn Gly Trp  
85 90 95  
Asn Leu Gly Tyr Leu His Cys Gln Val Ser Ala Phe Leu Met Gly Leu  
100 105 110  
Ser Val Ile Gly Ser Ile Leu Asn Ile Thr Gly Ile Ala Met Asn Arg  
115 120 125  
Tyr Cys Tyr Ile Cys His Ser Leu Lys Tyr Asp Lys Ile Tyr Ser Asn  
130 135 140  
Lys Asn Ser Leu Cys Tyr Val Phe Leu Ile Trp Met Leu Thr Leu Ile  
145 150 155 160  
Ala Ile Met Pro Asn Leu Gln Thr Gly Thr Leu Gln Tyr Asp Pro Arg  
165 170 175  
Ile Tyr Ser Cys Thr Phe Thr Gln Ser Val Ser Ala Tyr Thr Ile  
180 185 190  
Ala Val Val Val Phe His Phe Ile Val Pro Met Ile Ile Val Ile Phe  
195 200 205  
Cys Tyr Leu Arg Ile Trp Val Leu Val Leu Gln Val Arg Arg Arg Val  
210 215 220  
Lys Pro Asp Asn Lys Pro Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe  
225 230 235 240  
Val Thr Met Phe Val Val Phe Val Leu Phe Ala Ile Cys Trp Ala Pro  
245 250 255  
Leu Asn Leu Ile Gly Leu Ile Val Ala Ser Asp Pro Ala Thr Met Val  
260 265 270  
Pro Arg Ile Pro Glu Trp Leu Phe Val Ala Ser Tyr Tyr Leu Ala Tyr  
275 280 285  
Phe Asn Ser Cys Leu Asn Ala Ile Ile Tyr Gly Leu Leu Asn Gln Asn  
290 295 300  
Phe Arg Lys Glu Tyr Lys Lys Ile Ile Val Ser Leu Cys Thr Ala Lys  
305 310 315 320  
Met Phe Phe Val Glu Ser Ser Asn Glu Ala Asp Lys Ile Lys Cys  
325 330 335  
Lys Pro Ser Pro Leu Ile Pro Asn Asn Phe Leu Pro Val Asp Ser  
340 345 350  
Val

<210> 15  
<211> 1105  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> CDS  
<222> (13)...(1098)

<400> 15  
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                   Met Ser Glu Asn Gly Ser Ala Asn Cys Cys Glu Ala  
                   1                  5                  10

ggc ggg tgg gca gtg cgc ccg ggc tgg tcg ggg gct ggc agc gcg cg 99  
                   Gly Gly Trp Ala Val Arg Pro Gly Trp Ser Gly Ala Gly Ser Ala Arg  
                   15                  20                  25

ccc tcc agg acc cct cga cct ccc tgg gtg gct cca gcg ctg tcc gcg 147  
                   Pro Ser Arg Thr Pro Arg Pro Trp Val Ala Pro Ala Leu Ser Ala  
                   30                  35                  40                  45

gtg ctc atc gtc acc acc gcc gtg gac gtc gtg ggc aac ctc ctg gtg 195  
                   Val Leu Ile Val Thr Thr Ala Val Asp Val Val Gly Asn Leu Leu Val  
                   50                  55                  60

atc ctc tcc gtg ctc agg aac cgc aag ctc cgg aac gca ggt aat ttg 243  
                   Ile Leu Ser Val Leu Arg Asn Arg Lys Leu Arg Asn Ala Gly Asn Leu  
                   65                  70                  75

ttc ttg gtg agt ctg gca ttg gct gac ctg gtg gtc gcc ttc tac ccc 291  
                   Phe Leu Val Ser Leu Ala Leu Asp Leu Val Val Ala Phe Tyr Pro  
                   80                  85                  90

tac ccg cta atc ctc gtg gcc atc ttc tat gac ggc tgg gcc ctg ggg 339  
                   Tyr Pro Leu Ile Leu Val Ala Ile Phe Tyr Asp Gly Trp Ala Leu Gly  
                   95                  100                  105

gag gag cac tgc aag gcc agc gcc ttt gtg atg ggc ctg agc gtc atc 387  
                   Glu Glu His Cys Lys Ala Ser Ala Phe Val Met Gly Leu Ser Val Ile  
                   110                  115                  120                  125

ggc tct gtc ttc aat atc act gcc atc gcc att aac cgc tac tgc tac 435  
                   Gly Ser Val Phe Asn Ile Thr Ala Ile Ala Ile Asn Arg Tyr Cys Tyr  
                   130                  135                  140

atc tgc cac agc atg gcc tac cac cga atc tac cgg cgc tgg cac acc 483  
                   Ile Cys His Ser Met Ala Tyr His Arg Ile Tyr Arg Arg Trp His Thr  
                   145                  150                  155

cct ctg cac atc tgc ctc atc tgg ctc ctc acc gtg gtg gcc ttg ctg 531  
                   Pro Leu His Ile Cys Leu Ile Trp Leu Leu Thr Val Val Ala Leu Leu  
                   160                  165                  170

ccc aac ttc ttt gtg ggg tcc ctg gag tac gac cca cgc atc tat tcc 579  
                   Pro Asn Phe Phe Val Gly Ser Leu Glu Tyr Asp Pro Arg Ile Tyr Ser  
                   175                  180                  185

tgc acc ttc atc cag acc gcc agc acc cag tac acg gcg gca gtg gtg 627  
                   Cys Thr Phe Ile Gln Thr Ala Ser Thr Gln Tyr Thr Ala Ala Val Val  
                   190                  195                  200                  205

gtc atc cac ttc ctc ctc cct atc gct gtc gtg tcc ttc tgc tac ctg 675  
                   Val Ile His Phe Leu Leu Pro Ile Ala Val Val Ser Phe Cys Tyr Leu  
                   210                  215                  220

cgc atc tgg gtg ctg gtg ctt cag gcc cgc agg aaa gcc aag cca gag 723  
                   Arg Ile Trp Val Leu Val Leu Gln Ala Arg Arg Lys Ala Lys Pro Glu  
                   225                  230                  235

agc agg ctg tgc ctg aag ccc agc gac ttg cgg agc ttt cta acc atg Ser Arg Leu Cys Leu Lys Pro Ser Asp Leu Arg Ser Phe Leu Thr Met 240 245 250	771
ttt gtg gtg ttt gtg atc ttt gcc atc tgc tgg gct cca ctt aac tgc Phe Val Val Phe Val Ile Phe Ala Ile Cys Trp Ala Pro Leu Asn Cys 255 260 265	819
atc ggc ctc gct gtg gcc atc aac ccc caa gaa atg gct ccc cag atc Ile Gly Leu Ala Val Ala Ile Asn Pro Gln Glu Met Ala Pro Gln Ile 270 275 280 285	867
cct gag ggg cta ttt gtc act agc tac tta ctg gct tat ttc aac agc Pro Glu Gly Leu Phe Val Thr Ser Tyr Leu Leu Ala Tyr Phe Asn Ser 290 295 300	915
tgc ctg aat gcc att gtc tat ggg ctc ttg aac caa aac ttc cgc agg Cys Leu Asn Ala Ile Val Tyr Gly Leu Leu Asn Gln Asn Phe Arg Arg 305 310 315	963
gaa tac aag agg atc ctc ttg gcc ctt tgg aac cca cgg cac tgc att Glu Tyr Lys Arg Ile Leu Leu Ala Leu Trp Asn Pro Arg His Cys Ile 320 325 330	1011
caa gat gct tcc aag ggc agc cac gcg gag ggg ctg cag agc cca gct Gln Asp Ala Ser Lys Gly Ser His Ala Glu Gly Leu Gln Ser Pro Ala 335 340 345	1059
cca ccc atc att ggt gtg cag cac cag gca gat gct ctc tagcctg Pro Pro Ile Ile Gly Val Gln His Gln Ala Asp Ala Leu 350 355 360	1105

<210> 16  
 <211> 362  
 <212> PRT  
 <213> Homo sapiens

<400> 16

Met Ser Glu Asn Gly Ser Phe Ala Asn Cys Cys Glu Ala Gly Gly Trp	
1 5 10 15	
Ala Val Arg Pro Gly Trp Ser Gly Ala Gly Ser Ala Arg Pro Ser Arg	
20 25 30	
Thr Pro Arg Pro Pro Trp Val Ala Pro Ala Leu Ser Ala Val Leu Ile	
35 40 45	
Val Thr Thr Ala Val Asp Val Val Gly Asn Leu Leu Val Ile Leu Ser	
50 55 60	
Val Leu Arg Asn Arg Lys Leu Arg Asn Ala Gly Asn Leu Phe Leu Val	
65 70 75 80	
Ser Leu Ala Leu Ala Asp Leu Val Val Ala Phe Tyr Pro Tyr Pro Leu	
85 90 95	
Ile Leu Val Ala Ile Phe Tyr Asp Gly Trp Ala Leu Gly Glu Glu His	
100 105 110	
Cys Lys Ala Ser Ala Phe Val Met Gly Leu Ser Val Ile Gly Ser Val	
115 120 125	
Phe Asn Ile Thr Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His	
130 135 140	
Ser Met Ala Tyr His Arg Ile Tyr Arg Arg Trp His Thr Pro Leu His	
145 150 155 160	
Ile Cys Leu Ile Trp Leu Leu Thr Val Val Ala Leu Leu Pro Asn Phe	
165 170 175	

Phe Val Gly Ser Leu Glu Tyr Asp Pro Arg Ile Tyr Ser Cys Thr Phe  
 180 185 190  
 Ile Gln Thr Ala Ser Thr Gln Tyr Thr Ala Ala Val Val Val Ile His  
 195 200 205  
 Phe Leu Leu Pro Ile Ala Val Val Ser Phe Cys Tyr Leu Arg Ile Trp  
 210 215 220  
 Val Leu Val Leu Gln Ala Arg Arg Lys Ala Lys Pro Glu Ser Arg Leu  
 225 230 235 240  
 Cys Leu Lys Pro Ser Asp Leu Arg Ser Phe Leu Thr Met Phe Val Val  
 245 250 255  
 Phe Val Ile Phe Ala Ile Cys Trp Ala Pro Leu Asn Cys Ile Gly Leu  
 260 265 270  
 Ala Val Ala Ile Asn Pro Gln Glu Met Ala Pro Gln Ile Pro Glu Gly  
 275 280 285  
 Leu Phe Val Thr Ser Tyr Leu Leu Ala Tyr Phe Asn Ser Cys Leu Asn  
 290 295 300  
 Ala Ile Val Tyr Gly Leu Leu Asn Gln Asn Phe Arg Arg Glu Tyr Lys  
 305 310 315 320  
 Arg Ile Leu Leu Ala Leu Trp Asn Pro Arg His Cys Ile Gln Asp Ala  
 325 330 335  
 Ser Lys Gly Ser His Ala Glu Gly Leu Gln Ser Pro Ala Pro Pro Ile  
 340 345 350  
 Ile Gly Val Gln His Gln Ala Asp Ala Leu  
 355 360

<210> 17  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(5)  
 <223> Xaa = Any Amino Acid

<400> 17  
 Asn Ala Xaa Xaa Tyr  
 1 5

<210> 18  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Cys Tyr Ile Cys His Ser  
 1 5

<210> 19  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
 ctgtgcctct aagagccact tggtttc

27

<210> 20  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens

<400> 20	
tcctggat cctctccgtg ctca	24
<210> 21	
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<212> DNA	
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agccagatga ggcagatgtg caga	24
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<211> 24	
<212> DNA	
<213> Homo sapiens	
<400> 22	
tcctggatcat cctgtcggtg tatac	24
<210> 23	
<211> 24	
<212> DNA	
<213> Homo sapiens	
<400> 23	
ctgctgtaca gtttgtcgta cttg	24
<210> 24	
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<212> DNA	
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<400> 24	
gcaagagtgc gccctctact g	21
<210> 25	
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ggcctcactt gcctcctgca a	21
<210> 26	
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ctaattcctcg tggccaatct tctatg	26
<210> 27	
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<400> 27	
ttgggtgctga tgtcgatatt taaca	25
<210> 28	
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<213> Homo sapiens  
<400> 28  
cactgaactt ctgattcgca aactt 25  
<210> 29  
<211> 27  
<212> DNA  
<213> Homo sapiens  
<400> 29  
tattgaagac agagccgatg acgctca 27